

Amendments to the Claims under Revised 37 C.F.R. § 1.121

Claim 1 (currently amended): An isolated nucleic acid molecule comprising a nucleotide sequence ~~selected from the group consisting of:~~

- (a) ~~the nucleotide sequence as set forth in any of SEQ ID NO: 1, SEQ ID NO: 4, SEQ ID NO: 7, or SEQ ID NO: 11;~~
- (b) ~~the nucleotide sequence of the DNA insert in any of ATCC Deposit No[[s]]. PTA-961, PTA-962, PTA-963, or PTA-964;~~
- (c) ~~a nucleotide sequence encoding the polypeptide as set forth in any of SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 12; or~~
- (d) ~~a nucleotide sequence which hybridizes under moderately or highly stringent conditions to the complement of any of (a) - (c); and~~
- (e)(d) ~~a nucleotide sequence that is complementary to the nucleotide sequence of any of (a) - (c).~~

Claim 2 (currently amended): An isolated nucleic acid molecule comprising a nucleotide sequence ~~selected from the group consisting of:~~

- (a) ~~a nucleotide sequence encoding a polypeptide which that is at least about 70 percent identical to the polypeptide as set forth in any of SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 12, wherein the residue at position 95 is glutamic acid and the residues at positions 319-323 are glycine-lysine-lysine-alanine-lysine, and wherein the encoded polypeptide has an activity of the polypeptide set forth in any of SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 12;~~
- (b) ~~a nucleotide sequence encoding an allelic variant or splice variant of the nucleotide sequence as set forth in any of SEQ ID NO: 1, SEQ ID NO: 4, SEQ ID NO: 7, or SEQ ID NO: 11, the nucleotide sequence of the DNA insert in any of ATCC Deposit Nos. PTA-961, PTA-962, PTA-963, or PTA-964, or (a);~~
- (e)(b) a region of the nucleotide sequence of ~~any of SEQ ID NO: 1, SEQ ID NO: 4, SEQ ID NO: 7, or SEQ ID NO: 11, or~~ the DNA insert in any of ATCC Deposit No[[s]]. PTA-961, PTA-962, PTA-963, or PTA-964, (a), or (b) encoding a polypeptide fragment of SEQ ID NO: 8

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of at least about ~~25-377~~ amino acid residues, wherein the polypeptide fragment has an activity of the encoded polypeptide as set forth in any of SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 12, or is antigenic;

~~(d)(c)~~ a region of the nucleotide sequence of any of SEQ ID NO: 1, SEQ ID NO: 4, SEQ ID NO: 7, or SEQ ID NO: 11, or the DNA insert in any of ATCC Deposit No[[s]]. PTA-961, PTA-962, PTA-963, or PTA-964, or any of (a) - (e) comprising a fragment of at least about ~~16~~ 1131 nucleotides;

~~(e)~~ a nucleotide sequence which hybridizes under moderately or highly stringent conditions to the complement of any of (a) - (d); and

~~(f)(d)~~ a nucleotide sequence that is complementary to the nucleotide sequence of any of (a) - ~~(d)(c)~~.

Claim 3 (currently amended): An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence encoding a polypeptide as set forth in any of SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 12 with at least one conservative amino acid substitution, wherein the encoded polypeptide has an activity of the polypeptide set forth in any of SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 12;

(b) a nucleotide sequence encoding a polypeptide as set forth in any of SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 12 with at least one amino acid insertion, wherein the encoded polypeptide has an activity of the polypeptide set forth in any of SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 12;

(c) a nucleotide sequence encoding a polypeptide as set forth in any of SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 12 with at least one amino acid deletion, wherein the encoded polypeptide has an activity of the polypeptide set forth in any of SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 12;

~~(d)(b)~~ a nucleotide sequence encoding a polypeptide as set forth in any of SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 12 which has having a C- and/or N- terminal truncation, wherein the encoded polypeptide has an activity of the polypeptide set forth in any of

~~SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 12~~ comprises at least 377 amino acid residues;

~~(e)(c) a nucleotide sequence encoding a polypeptide as set forth in any of SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 12 with at least one modification selected from the group consisting of that is a conservative amino acid substitution[[s]], amino acid insertions, amino acid deletions, C-terminal truncation, and or N-terminal truncation, wherein the encoded polypeptide has an activity of the polypeptide set forth in any of SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 12 and~~ comprises at least 377 amino acid residues;

~~(f)(d) a nucleotide sequence of any the nucleotide sequence of (a) - (e) comprising a fragment of at least about 16 1131 nucleotides; or~~

~~(g) a nucleotide sequence which hybridizes under moderately or highly stringent conditions to the complement of any of (a) - (f); and~~

~~(h)(e) a nucleotide sequence that is complementary to the nucleotide sequence of any of (a) - (e)(d).~~

Claim 4 (original): A vector comprising the nucleic acid molecule of any of Claims 1, 2, or 3.

Claim 5 (original): A host cell comprising the vector of Claim 4.

Claim 6 (original): The host cell of Claim 5 that is a eukaryotic cell.

Claim 7 (original): The host cell of Claim 5 that is a prokaryotic cell.

Claim 8 (currently amended): A process of producing a ~~CHL~~ polypeptide encoded by the nucleic acid molecule of any of Claims 1, 2, or 3, comprising culturing the host cell of Claim 5 under suitable conditions to express the polypeptide, and optionally isolating the polypeptide from the culture.

Claim 9 (cancelled).

Claim 10 (currently amended): The process of Claim 8, wherein the nucleic acid molecule comprises promoter DNA other than the promoter DNA for the native CHL ~~polypeptide gene~~ operatively linked to the ~~DNA encoding the CHL polypeptide~~ nucleic acid molecule.

Claim 11 (currently amended): The isolated nucleic acid molecule according to Claim [[2]]3, wherein the percent identity of the encoded polypeptide is determined using a the BLASTP computer program ~~selected from the group consisting of GAP, BLASTN, FASTA, BLASTA, BLASTX, BestFit, and the Smith Waterman algorithm.~~

Claims 12-44 (cancelled).

Claim 45 (original): A viral vector comprising a nucleic acid molecule of any of Claims 1, 2, or 3.

Claims 46-56 (cancelled).

Claim 57 (new): An isolated nucleic acid molecule comprising a nucleotide sequence:

(a) encoding a polypeptide comprising the amino acid sequence as set forth in SEQ ID NO: 8;

wherein the methionine residue at either position 4 or 231 may be substituted with an isoleucine residue;

the leucine residue at either position 15 or 230 may be substituted with a valine residue;

the glutamic acid residue at position 28 may be substituted with an aspartic acid residue;

the methionine residue at either position 32 or 351 may be substituted with a valine residue;

the arginine residue at either position 43 or 366 may be substituted with a lysine residue;

the valine residue at position 77 may be substituted with a leucine residue;

the valine residue at position 101 may be substituted with a methionine residue;

the valine residue at position 124 may be substituted with an isoleucine residue;

the threonine residue at position 138 may be substituted with a serine residue;  
the serine residue at either position 184 or 348 may be substituted with an alanine residue;

the alanine residue at position 223 may be substituted with a serine residue;  
the isoleucine residue at position 309 may be substituted with a leucine residue;  
the glutamine residue at position 329 may be substituted with a lysine residue;  
the threonine residue at position 357 may be substituted with an alanine residue;  
the isoleucine residue at position 360 may be substituted with a valine residue; and  
the residues at any of positions 2, 8, 11, 13, 14, 16-19, 23, 76, 177, 186, 202, 205, 211, 218, 221, 270, 319-328, 336, or 350 may be substituted with any naturally occurring amino acid residue;

(b) encoding a polypeptide comprising residues 22 through 452 of the amino acid sequence as set forth in SEQ ID NO: 8;

wherein the glutamic acid residue at position 28 may be substituted with an aspartic acid residue;

the methionine residue at either position 32 or 351 may be substituted with a valine residue;

the arginine residue at either position 43 or 366 may be substituted with a lysine residue;  
the valine residue at position 77 may be substituted with a leucine residue;  
the valine residue at position 101 may be substituted with a methionine residue;  
the valine residue at position 124 may be substituted with an isoleucine residue;  
the threonine residue at position 138 may be substituted with a serine residue;  
the serine residue at either position 184 or 348 may be substituted with an alanine residue;

the alanine residue at position 223 may be substituted with a serine residue;  
the leucine residue at position 230 may be substituted with a valine residue;  
the methionine residue at position 231 may be substituted with an isoleucine residue;  
the isoleucine residue at position 309 may be substituted with a leucine residue;  
the glutamine residue at position 329 may be substituted with a lysine residue;  
the threonine residue at position 357 may be substituted with an alanine residue;

the isoleucine residue at position 360 may be substituted with a valine residue;  
the residues at any of positions 23, 76, 177, 186, 202, 205, 211, 218, 221, 270, 319-328,  
336, or 350 may be substituted with any naturally occurring amino acid residue;  
optionally further comprising an amino-terminal methionine; or  
(c) that is complementary to the nucleotide sequence of either (a) or (b).

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